

WTA #7

ENTERED



PCT10

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/069,427

DATE: 08/13/2002

TIME: 15:46:13

Input Set : A:\BB1395 USPCT Corrected Seq.txt
 Output Set: N:\CRF3\08132002\J069427.raw

3 <110> APPLICANT: Famodu, Omolayo O.
 4 Kinney, Anthony J.
 7 <120> TITLE OF INVENTION: Genes Encoding Sterol Delta-15 Reductase in Plants
 9 <130> FILE REFERENCE: BB1395 PCT
 11 <140> CURRENT APPLICATION NUMBER: 10/069,427
C--> 12 <141> CURRENT FILING DATE: 2002-07-16
 14 <150> PRIOR APPLICATION NUMBER: 60/156,820
 15 <151> PRIOR FILING DATE: 1999-09-30
 17 <160> NUMBER OF SEQ ID NOS: 10
 19 <170> SOFTWARE: Microsoft Office 95
 21 <210> SEQ ID NO: 1
 22 <211> LENGTH: 427
 23 <212> TYPE: DNA
 24 <213> ORGANISM: Glycine max
 26 <220> FEATURE:
 27 <221> NAME/KEY: unsure
 28 <222> LOCATION: (360)
 29 <223> OTHER INFORMATION: n=a,c,g or t
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 33 aactccgttc ctttgcgtgt ggggttcttc acttacttgg ccgttgctgg atccattctc 120
 34 cctggaaaac ttgttccctgg ctttgcacta ctcgatggaa ctcgtctaca ctattgctgc 180
 35 aatggctctgc ttcgcgttct tctgttgggt gcacttctcg ggatcggtgc caagatgggt 240
 36 ttgtgtctc ccactgccat atcaaacaga ggacttgagc tgctgtccac aactttgcc 300
W--> 37 ttcagtttc ttgttaaccct gatattgcat ttttccgggt gcaagtca aagtaaaggn 360
 38 tcatcaactaa agcctcatct cagtggAAC ctgatacacg attggtggtt tggaaataca 420
 39 actaaaa 427
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 43 <211> LENGTH: 126
 44 <212> TYPE: PRT
 45 <213> ORGANISM: Glycine max
 47 <400> SEQUENCE: 2
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 49 1 5 10 15
 51 Phe Phe Thr Tyr Leu Ala Val Ala Gly Ser Ile Leu Pro Gly Lys Leu
 52 20 25 30
 54 Val Pro Gly Val Ala Leu Leu Asp Gly Thr Arg Leu His Tyr Cys Cys
 55 35 40 45
 57 Asn Gly Leu Leu Ser Leu Leu Leu Val Ala Leu Leu Gly Ile Gly
 58 50 55 60
 60 Ala Lys Met Gly Phe Val Ser Pro Thr Ala Ile Ser Asn Arg Gly Leu
 61 65 70 75 80
 63 Glu Leu Leu Ser Thr Thr Phe Ala Phe Ser Phe Leu Val Thr Leu Ile

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64	85	90	95	
66	Leu His Phe Ser Gly Cys Lys Ser Gln Ser Lys Gly Ser Ser Leu Lys			
67	100	105	110	
69	Pro His Leu Ser Gly Asn Leu Ile His Asp Trp Trp Phe Gly			
70	115	120	125	
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74	<211> LENGTH: 1631			
75	<212> TYPE: DNA			
76	<213> ORGANISM: Glycine max			
78	<400> SEQUENCE: 3			
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80	ctcaactcgaa gtgatgatgg agtcacacgt ggatcttaggt tttctccctc aagctctcac	120		
81	tccatcttgg aactccgttc cttgttgtt ggggttcttc acttacttgg ccgttgctgg	180		
82	atccattctc cctggaaaac ttgttccctgg cgttgcacta ctcgatggaa ctcgtctaca	240		
83	ctattgctgc aatggctgtc ttcgtcttc tctgttgggt gcacttctcg ggatcggtgc	300		
84	caagatgggt tttgtgtc tcactgccat atcagacaga ggacttgagc tgctgtccac	360		
85	aacttttgc ttcagtttc ttgttaaccct gatattgcatt tttccgggtt gcaagtacaca	420		
86	aagtaaaggt tcatactaa agcctcatct cagtggaaac ctgatacacg attgggtt	480		
87	tggtatacaa ctaaatccac agttcatggg tatcgacctc aaattttct ttgttagagc	540		
88	tggaaatgatg ggtggctac ttatcaattt atctatttctt atgaagagca ttcaagatgg	600		
89	tactttggc cagtcaatga ttctctacca gctattctgt gcactataca tcctggacta	660		
90	ttttgtacat gaagagtaca tgacatccac ctgggacata attgcagaga gactgggctt	720		
91	catgttggc tttggagatt tagtgtggat tccttcttc ttcaagatgg agggatgggt	780		
92	gctcttgatg aacagtgtgg agttaaacacc agtgcattt gtagctaatt gctttgtt	840		
93	cctgatttggc tacatgttat ttgcaggagc aaacaagcaa aagcatgtgt tcaaaaagaa	900		
94	tccaaaggct cctatctggg gtaagcctcc aaaagtctt ggtggaaagc tacttgcctc	960		
95	tggttattgg ggtattgtca gacactgtaa ttaccttaggg gatttgatgc ttgctctctc	1020		
96	ctttagctt ccatgtggaa taagttcacc aattccatac ttctatccaa tttatcttct	1080		
97	tattctgtta atctggagag agagaaggaa tgaagtcgt tgccggaga agtatacgaa	1140		
98	gatatggcc gatgtatgtc aacttgcattt atggagaata ttgccttacg tttattagga	1200		
99	tgaaaaaaaaa aagggtttca ccatgaattt ttcatcttgc cgatgttatt aagcacttcg	1260		
100	atgtaaattt gttctgttc ttgtgggtt aatcttggat ctttcttatt tgagccatgt	1320		
101	agctgcagga gagtgtttcg agggatttat ttaccatct atatttgcgtt atcattatgc	1380		
102	tgcagcctgc aggccattcat ttttcaatgg ccaactcttt ttgacttgc ttatgtt	1440		
103	ttagatgaga atttcatgtt caaagctcctt aggctaaaaaa aaacagtgtc atgttctatg	1500		
104	gaaagtgcag gaagcaattt ggggactgca ggaagcaattt gccttacat tgatatgctc	1560		
105	aatggtactt taggcctttt aatgttcttgc ttttcattt gtgagttattt attggccccaa	1620		
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110	<211> LENGTH: 374			
111	<212> TYPE: PRT			
112	<213> ORGANISM: Glycine max			
114	<400> SEQUENCE: 4			
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116	1 5 10 15			
118	Pro Ser Trp Asn Ser Val Pro Leu Leu Val Gly Phe Phe Thr Tyr Leu			
119	20 25 30			
121	Ala Val Ala Gly Ser Ile Leu Pro Gly Lys Leu Val Pro Gly Val Ala			
122	35 40 45			

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Input Set : A:\BB1395 USPCT Corrected Seq.txt
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124 Leu Leu Asp Gly Thr Arg Leu His Tyr Cys Cys Asn Gly Leu Leu Ser
125      50          55          60
127 Leu Leu Leu Leu Val Ala Leu Leu Gly Ile Gly Ala Lys Met Gly Phe
128      65          70          75          80
130 Val Ser Pro Thr Ala Ile Ser Asp Arg Gly Leu Glu Leu Leu Ser Thr
131      85          90          95
133 Thr Phe Ala Phe Ser Phe Leu Val Thr Leu Ile Leu His Phe Ser Gly
134      100         105         110
136 Cys Lys Ser Gln Ser Lys Gly Ser Ser Leu Lys Pro His Leu Ser Gly
137      115         120         125
139 Asn Leu Ile His Asp Trp Trp Phe Gly Ile Gln Leu Asn Pro Gln Phe
140      130         135         140
142 Met Gly Ile Asp Leu Lys Phe Phe Phe Val Arg Ala Gly Met Met Gly
143 145      150         155         160
145 Trp Leu Leu Ile Asn Leu Ser Ile Leu Met Lys Ser Ile Gln Asp Gly
146      165         170         175
148 Thr Leu Ser Gln Ser Met Ile Leu Tyr Gln Leu Phe Cys Ala Leu Tyr
149      180         185         190
151 Ile Leu Asp Tyr Phe Val His Glu Glu Tyr Met Thr Ser Thr Trp Asp
152      195         200         205
154 Ile Ile Ala Glu Arg Leu Gly Phe Met Leu Val Phe Gly Asp Leu Val
155      210         215         220
157 Trp Ile Pro Phe Ser Phe Ser Ile Gln Gly Trp Trp Leu Leu Met Asn
158 225      230         235         240
160 Ser Val Glu Leu Thr Pro Ala Ala Ile Val Ala Asn Cys Phe Val Phe
161      245         250         255
163 Leu Ile Gly Tyr Met Val Phe Arg Gly Ala Asn Lys Gln Lys His Val
164      260         265         270
166 Phe Lys Lys Asn Pro Lys Ala Pro Ile Trp Gly Lys Pro Pro Lys Val
167      275         280         285
169 Ile Gly Gly Lys Leu Leu Ala Ser Gly Tyr Trp Gly Ile Ala Arg His
170      290         295         300
172 Cys Asn Tyr Leu Gly Asp Leu Met Leu Ala Leu Ser Phe Ser Leu Pro
173 305      310         315         320
175 Cys Gly Ile Ser Ser Pro Ile Pro Tyr Phe Tyr Pro Ile Tyr Leu Leu
176      325         330         335
178 Ile Leu Leu Ile Trp Arg Glu Arg Arg Asp Glu Ala Arg Cys Ala Glu
179      340         345         350
181 Lys Tyr Arg Glu Ile Trp Ala Glu Tyr Arg Lys Leu Val Pro Trp Arg
182      355         360         365
184 Ile Leu Pro Tyr Val Tyr
185      370
188 <210> SEQ ID NO: 5
189 <211> LENGTH: 667
190 <212> TYPE: DNA
191 <213> ORGANISM: Zea mays
193 <400> SEQUENCE: 5
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195 atctttctta ttggctacct agtgttccga ggagctaaca agcaaaaaca tgtgttcaag 120

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196 aaggacccca aagctcctat atggggaaaa cctcccaaag ttgtcgaaaa aaagctacta 180
 197 gcatctgggt actggggcat cgcaaggcac tgcaattatac tcggagacct gctgcttagca 240
 198 cttcgttca gcttgcctg tggagtgaat tccgtggtcc catacttcta ccccacgtac 300
 199 ctgctcattt tactgttctt gagggaaagg cgcgatgagg cgagggtgctc gcagaagtac 360
 200 agggagatct gggcagagta ctgcaagctc gtgccgtgga gatcctgtcc ttatgtgtac 420
 201 tgaagagacg gtagaaacca aggcaagctca tggccctggg ccagctgtaa accttatttt 480
 202 gtttgcctt aaccagttgg tgaatgttga ttagactc gttaaactgt gaccgtgcaa 540
 203 acttttgtta ttgttggtcc atacatgttt ggaatcgtga atcagaccgc ctcacttgg 600
 204 ggcaaa 660
 205 aaa 667
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 209 <211> LENGTH: 140
 210 <212> TYPE: PRT
 211 <213> ORGANISM: Zea mays
 213 <400> SEQUENCE: 6
 214 Pro Arg Val Arg Lys Asn Lys Val Glu Leu Ser Leu Leu Ser Gly Leu
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 217 Ala Asn Leu Cys Ile Phe Leu Ile Gly Tyr Leu Val Phe Arg Gly Ala
 218 20 25 30
 220 Asn Lys Gln Lys His Val Phe Lys Lys Asp Pro Lys Ala Pro Ile Trp
 221 35 40 45
 223 Gly Lys Pro Pro Lys Val Val Gly Gly Lys Leu Leu Ala Ser Gly Tyr
 224 50 55 60
 226 Trp Gly Ile Ala Arg His Cys Asn Tyr Leu Gly Asp Leu Leu Leu Ala
 227 65 70 75 80
 229 Leu Ser Phe Ser Leu Pro Cys Gly Val Ser Ser Val Val Pro Tyr Phe
 230 85 90 95
 232 Tyr Pro Thr Tyr Leu Leu Ile Leu Val Leu Arg Glu Arg Arg Asp
 233 100 105 110
 235 Glu Ala Arg Cys Ser Gln Lys Tyr Arg Glu Ile Trp Ala Glu Tyr Cys
 236 115 120 125
 238 Lys Leu Val Pro Trp Arg Ile Leu Pro Tyr Val Tyr
 239 130 135 140
 242 <210> SEQ ID NO: 7
 243 <211> LENGTH: 1364
 244 <212> TYPE: DNA
 245 <213> ORGANISM: Glycine max
 247 <400> SEQUENCE: 7
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 249 gtgatgtgg agtcacacgt ggatctagg tttctccttc aagctctcac tccatcttgg 120
 250 aactccgttc ctttgcgtgt ggggttcttc acttacttgg cggttgcgtgg atccattctc 180
 251 cctggaaaaac ttgttccctgg cggtgcacta ctgcgtggaa ctgcgtctaca ctattgtgc 240
 252 aatggtctgc tctcgcttct tctgttgggt gcacttctcg ggatcgggtgc caagatgggt 300
 253 ttgtgtctc ccactgcccattt atcagacaga ggacttgagc tgctgtccac aactttgcc 360
 254 ttcagtttc ttgttaaccct gatattgcat tttccgggtt gcaagtccaca aagtaaagg 420
 255 tcatcaactaa agcctcatct cagtgaaac ctgatacacg attgggtgggt tggtatacaa 480
 256 ctaaatccac agttcatggg tatcgacccaa aagctggaa tggatggatg gctacttatac 540
 257 aatttatcta ttcttatgaa gggcattcaa gatggtaactt tgagccagtc aatgattctc 600
 258 taccagctat tctgtgcact atacatcctg gactatggtaactt tacatgaaga gtacatgaca 660

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Input Set : A:\BB1395 USPCT Corrected Seq.txt
Output Set: N:\CRF3\08132002\J069427.raw

259	tccacctggg	acataattgc	agagagactg	ggcttcatgt	tggctttgg	agatttagt	720
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261	acaccagctg	ccatttgc	taattgcctt	gtgttcctga	ttggatacat	gttatttcga	840
262	ggagcaaaca	agcaaaagca	tgtgttcaaa	aagaatccaa	aggctcctat	ctggggtaag	900
263	cctccaaaag	tcatttgcgg	aaagctactt	gcttctggtt	attggggtat	tgctagacac	960
264	tgttaattacc	tagggattt	gatgttgc	ctctccttta	gcttaccatg	tgggataagt	1020
265	tcaccaattc	catacttcta	tccaatttat	tttcttattc	tgttaatctg	gagagagaga	1080
266	acggatgaag	ctcggtgcgc	cgagaagtat	agagagatat	gggccgagta	tcgtaaactt	1140
267	gttccatgga	aatattgc	ttacgtttat	tagatgaaa	aaaaaaaggg	cttcaccatg	1200
268	aattcttcat	tttgcgtat	ttattaagca	cttcgtatgta	aattggttct	tgttcttgc	1260
269	gttcaatct	tggatcttt	cttatttgc	catgtatgt	caggagatg	tttcgaggga	1320
270	tttatcttac	catctatatt	tgtgtaaaaa	aaaaaaa	aaaaaaa		1364
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274	<211>	LENGTH:	369				
275	<212>	TYPE:	PRT				
276	<213>	ORGANISM:	Glycine max				
278	<400>	SEQUENCE:	8				
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282	Pro Ser Trp Asn Ser Val Pro Leu Leu Val Gly Phe Phe Thr Tyr Leu						
283	20	25	30				
285	Ala Val Ala Gly Ser Ile Leu Pro Gly Lys Leu Val Pro Gly Val Ala						
286	35	40	45				
288	Leu Leu Asp Gly Thr Arg Leu His Tyr Cys Cys Asn Gly Leu Leu Ser						
289	50	55	60				
291	Leu Leu Leu Val Ala Leu Leu Gly Ile Gly Ala Lys Met Gly Phe						
292	65	70	75	80			
294	Val Ser Pro Thr Ala Ile Ser Asp Arg Gly Leu Glu Leu Leu Ser Thr						
295	85	90	95				
297	Thr Phe Ala Phe Ser Phe Leu Val Thr Leu Ile Leu His Phe Ser Gly						
298	100	105	110				
300	Cys Lys Ser Gln Ser Lys Gly Ser Ser Leu Lys Pro His Leu Ser Gly						
301	115	120	125				
303	Asn Leu Ile His Asp Trp Trp Phe Gly Ile Gln Leu Asn Pro Gln Phe						
304	130	135	140				
306	Met Gly Ile Asp Leu Lys Ala Gly Met Met Gly Trp Leu Leu Ile Asn						
307	145	150	155	160			
309	Leu Ser Ile Leu Met Lys Ser Ile Gln Asp Gly Thr Leu Ser Gln Ser						
310	165	170	175				
312	Met Ile Leu Tyr Gln Leu Phe Cys Ala Leu Tyr Ile Leu Asp Tyr Phe						
313	180	185	190				
315	Val His Glu Glu Tyr Met Thr Ser Thr Trp Asp Ile Ile Ala Glu Arg						
316	195	200	205				
318	Leu Gly Phe Met Leu Val Phe Gly Asp Leu Val Trp Ile Pro Phe Ser						
319	210	215	220				
321	Phe Ser Ile Gln Gly Trp Trp Leu Leu Met Asn Ser Val Glu Leu Thr						
322	225	230	235	240			
324	Pro Ala Ala Ile Val Ala Asn Cys Phe Val Phe Leu Ile Gly Tyr Met						
325	245	250	255				

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:1; N Pos. 360

VERIFICATION SUMMARY

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L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:37 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:300